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## RAW SEQUENCE LISTING

DATE: 12/19/2001

PATENT APPLICATION: US/09/938,703

TIME: 12:44:35

Input Set : N:\Crf3\RULE60\09938703.txt

Output Set: N:\CRF3\12192001\I938703.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: SAMSON, MICHEL

6 PARMENTIER, MARC

7 VASSART, GILBERT

8 LIBERT, FREDERICK

10 (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

11 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

13 (iii) NUMBER OF SEQUENCES: 17

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Knobbe, Martens, Olson &amp; Bear

17 (B) STREET: 620 Newport Center Drive 16th Floor

18 (C) CITY: Newport Beach

19 (D) STATE: CA

20 (E) COUNTRY: U.S.A.

21 (F) ZIP: 92660

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

29 (vi) CURRENT APPLICATION DATA:

C--&gt; 30 (A) APPLICATION NUMBER: US/09/938,703

C--&gt; 31 (B) FILING DATE: 24-Aug-2001

32 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/626,939

37 (B) FILING DATE: 2000-07-27

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Altman, Daniel E

44 (B) REGISTRATION NUMBER: 34,115

45 (C) REFERENCE/DOCKET NUMBER:

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 792 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

58 (ix) FEATURE:

59 (A) NAME/KEY: CDS

60 (B) LOCATION: 240..791

63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

65	GAATTC	CCCC	AACAGAG	CCCA	AGCTCT	CCAT	CTAGTGG	ACA	GGGAAG	CTAG	CAGCAA	ACCT	60			
66	TCCCTT	CACT	ACAAA	ACTT	ATTGCT	TGGC	CAAAA	AAGA	GTTAAT	TCAA	TGTAG	ACATC	120			
67	TATGT	AGGCA	ATTAAA	AACC	TATTG	ATGTA	TAAA	ACAG	TTCAT	TATG	GAGGG	CAACT	180			
68	AAATAC	ATT	C	TAGG	ACTT	TA	TAAA	GAT	CA	CTTTT	TATTT	ATGC	ACAGG	TGGA	ACAAG	239

ENTERED

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```

69 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA      287
70 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
71   1           5           10           15
72 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      335
73 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
74           20           25           30
75 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      383
76 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
77           35           40           45
78 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      431
79 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
80   50           55           60
81 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      479
82 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
83  65           70           75           80
84 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT      527
85 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
86           85           90           95
87 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      575
88 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
89           100          105          110
90 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG      623
91 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
92           115          120          125
93 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT      671
94 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
95           130          135          140
96 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT      719
97 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
98 145          150          155          160
99 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC      767
100 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
101           165          170          175
102 ACC TGC AGC TCT CAT TTT CCA TAC A      792
103 Thr Cys Ser Ser His Phe Pro Tyr
104           180
107 (2) INFORMATION FOR SEQ ID NO: 2:
109   (i) SEQUENCE CHARACTERISTICS:
110       (A) LENGTH: 1477 base pairs
111       (B) TYPE: nucleic acid
112       (C) STRANDEDNESS: single
113       (D) TOPOLOGY: linear
115   (ii) MOLECULE TYPE: DNA (genomic)
118   (ix) FEATURE:
119       (A) NAME/KEY: CDS
120       (B) LOCATION: 240..1295
123   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
125 GAATTC-----AACAGAGCCA AGCTCTCCAT CTAGTGGACA GCGAAGCTAG CAGCAAACCT      60
126 TCCCTTCACT ACAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC      120

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127	TATGTAGGCA	ATTAAAAACC	TATTGATGTA	TAAAACAGTT	TGCATTTCATG	GAGGGCAACT	180
128	AAATACATTC	TAGGACTTTA	TAAAAGATCA	CTTTTTATTT	ATGCACAGGG	TGGAACAAG	239
129	ATG GAT TAT	CAA GTG TCA	AGT CCA ATC	TAT GAC ATC	AAT TAT TAT	ACA	287
130	Met Asp Tyr	Gln Val Ser	Ser Pro Ile	Tyr Asp Ile	Asn Tyr Tyr	Thr	
131	1	5	10	15			
132	TCG GAG CCC	TGC CAA AAA	ATC AAT GTG	AAG CAA ATC	GCA GCC CGC	CTC	335
133	Ser Glu Pro	Cys Gln Lys	Ile Asn Val	Lys Gln Ile	Ala Ala Arg	Leu	
134		20	25	30			
135	CTG CCT CCG	CTC TAC TCA	CTG GTG TTC	ATC TTT GGT	TTT GTG GGC	AAC	383
136	Leu Pro Pro	Leu Tyr Ser	Leu Val Phe	Ile Phe Gly	Phe Val Gly	Asn	
137		35	40	45			
138	ATG CTG GTC	ATC CTC ATC	CTG ATA AAC	TGC AAA AGG	CTG AAG AGC	ATG	431
139	Met Leu Val	Ile Leu Ile	Leu Ile Asn	Cys Lys Arg	Leu Lys Ser	Met	
140	50	55	60				
141	ACT GAC ATC	TAC CTG CTC	AAC CTG GCC	ATC TCT GAC	CTG TTT TTC	CTT	479
142	Thr Asp Ile	Tyr Leu Leu	Asn Leu Ala	Ile Ser Asp	Leu Phe Phe	Leu	
143	65	70	75	80			
144	CTT ACT GTC	CCC TTC TGG	GCT CAC TAT	GCT GCC GCC	CAG TGG GAC	TTT	527
145	Leu Thr Val	Pro Phe Trp	Ala His Tyr	Ala Ala Ala	Gln Trp Asp	Phe	
146		85	90	95			
147	GGA AAT ACA	ATG TGT CAA	CTC TTG ACA	GGG CTC TAT	TTT ATA GGC	TTC	575
148	Gly Asn Thr	Met Cys Gln	Leu Leu Thr	Gly Leu Tyr	Phe Ile Gly	Phe	
149		100	105	110			
150	TTC TCT GGA	ATC TTC TTC	ATC ATC CTC	CTG ACA ATC	GAT AGG TAC	CTG	623
151	Phe Ser Gly	Ile Phe Phe	Ile Ile Leu	Leu Thr Ile	Asp Arg Tyr	Leu	
152		115	120	125			
153	GCT GTC GTC	CAT GCT GTG	TTT GCT TTA	AAA GCC AGG	ACG GTC ACC	TTT	671
154	Ala Val Val	His Ala Val	Phe Ala Leu	Lys Ala Arg	Thr Val Thr	Phe	
155	130	135	140				
156	GGG GTG GTG	ACA AGT GTG	ATC ACT TGG	GTG GTG GCT	GTG TTT GCG	TCT	719
157	Gly Val Val	Thr Ser Val	Ile Thr Trp	Val Val Ala	Val Phe Ala	Ser	
158	145	150	155	160			
159	CTC CCA GGA	ATC ATC TTT	ACC AGA TCT	CAA AAA GAA	GGT CTT CAT	TAC	767
160	Leu Pro Gly	Ile Ile Phe	Thr Arg Ser	Gln Lys Glu	Gly Leu His	Tyr	
161		165	170	175			
162	ACC TGC AGC	TCT CAT TTT	CCA TAC AGT	CAG TAT CAA	TTC TGG AAG	AAT	815
163	Thr Cys Ser	Ser His Phe	Pro Tyr Ser	Gln Tyr Gln	Phe Trp Lys	Asn	
164		180	185	190			
165	TTC CAG ACA	TTA AAG ATA	GTC ATC TTG	GGG CTG GTC	CTG CCG CTG	CTT	863
166	Phe Gln Thr	Leu Lys Ile	Val Ile Leu	Gly Leu Val	Leu Pro Leu	Leu	
167		195	200	205			
168	GTC ATG GTC	ATC TGC TAC	TCG GGA ATC	CTA AAA ACT	CTG CTT CGG	TGT	911
169	Val Met Val	Ile Cys Tyr	Ser Gly Ile	Leu Lys Thr	Leu Leu Arg	Cys	
170	210	215	220				
171	CGA AAT GAG	AAG AAG AGG	CAC AGG GCT	GTG AGG CTT	ATC TTC ACC	ATC	959
172	Arg Asn Glu	Lys Lys Arg	His Arg Ala	Val Arg Leu	Ile Phe Thr	Ile	
173	225	230	235	240			
174	ATG ATT GTT	TAT TTT CTC	TTC TGG GCT	CCC TAC AAC	ATT GTC CTT	CTC	1007
175	Met Ile Val	Tyr Phe Leu	Phe Trp Ala	Pro Tyr Asn	Ile Val Leu	Leu	

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176          245          250          255
177 CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT      1055
178 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
179          260          265          270
180 AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG      1103
181 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
182          275          280          285
183 CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC      1151
184 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
185          290          295          300
186 AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC      1199
187 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
188 305          310          315          320
189 TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC      1247
190 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
191          325          330          335
192 TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG      1295
193 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
194          340          345          350
195 TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTTCA      1355
196 TACACAGCCT GGGCTGGGGG TNGGTTGGNN GAGGTCTTTT TAAAAAGGAA GTTACTGTTA      1415
197 TAGAGGGTCT AAGATTCATC CATTTATTTG GCATCTGTTT AAAGTAGATT AGATCCGAAT      1475
198 TC      1477
201 (2) INFORMATION FOR SEQ ID NO: 3:
203   (i) SEQUENCE CHARACTERISTICS:
204       (A) LENGTH: 1442 base pairs
205       (B) TYPE: nucleic acid
206       (C) STRANDEDNESS: single
207       (D) TOPOLOGY: linear
209   (ii) MOLECULE TYPE: DNA (genomic)
212   (ix) FEATURE:
213       (A) NAME/KEY: CDS
214       (B) LOCATION: 240..884
217   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
219 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT      60
220 TCCCTTCACT ACAAACCTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC      120
221 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAACAGTT TGCATTCATG GAGGGCAACT      180
222 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG      239
223 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA      287
224 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
225 1          5          10          15
226 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      335
227 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
228          20          25          30
229 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      383
230 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
231          35          40          45
232 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      431
233 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met

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```

234      50      55      60
235 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      479
236 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
237 65      70      75      80
238 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT      527
239 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
240      85      90      95
241 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      575
242 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
243      100      105      110
244 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG      623
245 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
246      115      120      125
247 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT      671
248 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
249      130      135      140
250 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT      719
251 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
252 145      150      155      160
253 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC      767
254 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
255      165      170      175
256 ACC TGC AGC TCT CAT TTT CCA TAC ATT AAA GAT AGT CAT CTT GGG GCT      815
257 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala
258      180      185      190
259 GGT CCT GCC GCT GCT TGT CAT GGT CAT CTG CTA CTC GGG AAT CCT AAA      863
260 Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys
261      195      200      205
262 AAC TCT GCT TCG GTG TCG AAA TGAGAAGAAG AGGCACAGGG CTGTGAGGCT      914
263 Asn Ser Ala Ser Val Ser Lys
264      210      215
265 TATCTTCACC ATCATGATTG TTTATTTTCT CTTCTGGGCT CCCTACAACA TTGTCCTTCT      974
266 CCTGAACACC TTCCAGGAAT TCTTTGGCCT GAATAATTGC AGTAGCTCTA ACAGGTTGGA      1034
267 CCAAGCTATG CAGGTGACAG AGACTCTTGG GATGACGCAC TGCTGCATCA ACCCCATCAT      1094
268 CTATGCCTTT GTCGGGGAGA AGTTCAGAAA CTACCTCTTA GTCTTCTTCC AAAAGCACAT      1154
269 TGCCAAACGC TTCTGCAAAT GCTGTTCTAT TTTCCAGCAA GAGGCTCCCG AGCGAGCAAG      1214
270 CTCAGTTTAC ACCCGATCCA CTGGGGAGCA GGAAATATCT GTGGGCTTGT GACACGGACT      1274
271 CAAGTGGGCT GGTGACCCAG TCAGAGTTGT GCACATGGCT TAGTTTTTCAT ACACAGCCCTG      1334
272 GGCTGGGGGT GGTGGGGAGG TCTTTTTTAA AAGGAAGTTA CTGTTATAGA GGGTCTAAGA      1394
273 TTCATCCATT TATTTGGCAT CTGTTTAAAG TAGATTAGAT CCGAATTC      1442
276 (2) INFORMATION FOR SEQ ID NO: 4:
277 (i) SEQUENCE CHARACTERISTICS:
278 (A) LENGTH: 184 amino acids
279 (B) TYPE: amino acid
280 (D) TOPOLOGY: linear
281 (ii) MOLECULE TYPE: protein
282 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
287 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
288 1 5 10 15

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/938,703

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Input Set : N:\Crif3\RULE60\09938703.txt

Output Set: N:\CRF3\12192001\I938703.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:418 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:536 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10